



Blast 2 Sequences results

PubMed

Entrez

BLAST

OMIM

Taxonomy

Structure

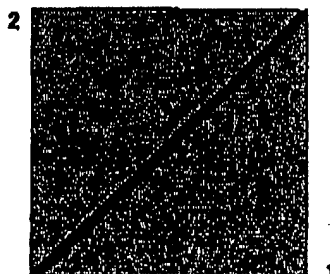
BLAST 2 SEQUENCES RESULTS VERSION BLASTP 2.2.3 [Apr-24-2002]

Matrix: BLOSUM62 gap opens: 11 gap extension: 1
 x_dropoff: 30 expect: 10.00 wordsize: 3 Filter: ☐ Align: ☐

Sequence 1 gi 4140289

Length 215 (1..215)

Sequence 2 gi 123369 High mobility group protein 1 (HMG-1). Length 215 (1..215)



NOTE: The statistics (bitscore and expect value) is calculated based on the size of nr database

Score = 415 bits (1067). Expect = e-115
 Identities = 195/215 (90%), Positives = 209/215 (96%)

```

Query:      1  MGKGDPPKPRGKMSSYAFFVQTCREEHKKKHPDASVNFSEFSKKCSERWKTMSKEKGKF 60
Sbjct:      1  MGKGDPPKPRGKMSSYAFFVQTCREEHKKKHPDASVNFSEFSKKCSERWKTMS+KEKGKF 60
dna-binding 9  *****
HMG1        1  ++++++

Query:      61  EDMAKADKLRYEKEMKNYVPPKGETKKKFKDPNAPKRPPSAFFLCSEFRPKIKGEHPGL 120
Sbjct:      61  EDMAKADK RYE+EMK Y+PPKGETKKKFKDPNAPKRPPSAFFLCSE+RPKIKGEHPGL 120
dna-binding 95  EDMAKADKARYEREMKTYIPPKGETKKKFKDPNAPKRPPSAFFLCSEYRPKIKGEHPGL 120
dna-binding 61  *****
HMG1        61  ++++++

Query:     121  SIGDVAKKL GEMWNNTAADDKQPYEKKAALKKEKYEKDI AAYRAKGKVDAGKKVAKAEK 180
Sbjct:     121  SIGDVAKKL GEMWNNTAADDKQPYEKKAALKKEKYEKDI AAYRAKGK DA KK V KAEK
dna-binding 121  SIGDVAKKL GEMWNNTAADDKQPYEKKAALKKEKYEKDI AAYRAKGK PDAAKGVVAKAEK 180
HMG1       121  *****

Query:     181  SKKKKEEEDEDEDEDEDEDEDEDEDEDEDEDEDEDEDEDEDEDEDEDEDEDEDEDE 215
Sbjct:     181  SKKKKEEEDE+++E++EE+E+EE+E+EE+DDDE 215
ASP/GLU-RICH (ACIDIC). 186  SKKKKEEEDEDEDEDEDEDEDEDEDEDEDEDEDEDEDEDEDEDEDEDEDEDEDEDE 215
HMG1       181  *****

```

CPU time: 0.03 user secs. 0.06 sys. secs 0.09 total secs.

Lambda K H
 0.304 0.127 0.357

Gapped
 Lambda K H
 0.267 0.0410 0.140

Matrix: BLOSUM62
 Gap Penalties: Existence: 11, Extension: 1
 Number of Hits to DB: 5441



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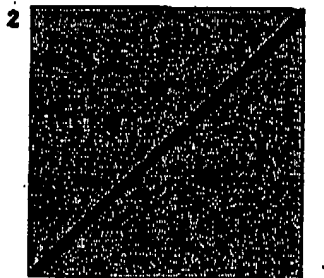
OMIM

Taxonomy

Structure

BLAST 2 SEQUENCES RESULTS VERSION BLASTP 2.2.3 [Apr-24-2002]

Matrix: **BLOSUM82** gap open: **11** gap extension: **1**
 x_dropoff: **30** expect: **10.00** wordsize: **3** Filter ☐ Align ☐

Sequence 1 [gi_123373](#) High mobility group protein 2 (HMG-2). Length 207 (1..207)Sequence 2 [gi_123374](#) High mobility group protein 2 (HMG-2). Length 209 (1..209)

NOTE: The statistics (bitscore and expect value) is calculated based on the size of nr database

Score = 402 bits (1034), Expect = e-112
 Identities = 188/207 (90%), Positives = 201/207 (96%)

```

Query:          1  MGKGDPNKPRGKISSYAFVQTCREEHKKKHPDSSVNFAEFSRKCSERWKTMSKEKGKF 60
Sbjct:          1  MGKGDPNKPRGKISSYAFVQTCREEHKKKHPDSSVNFAEFS+KCSERWKTMS+KEK  KF
dna-binding     9  MGKGDPNKPRGKISSYAFVQTCREEHKKKHPDSSVNFAEFSKKCSERWKTMSAKEKSKF 60
HMG2            1  *****
                1  ++++++

Query:          61  EEMAKGDKARYDREMKNYVPPKGEKKGKKKDPNAPKRPPSAFFLCSEHRPKIKNDHPGL 120
Sbjct:          61  E+MAK  DKARYDREMKNYVPPKG+KKGKKKDPNAPKRPPSAFFLCSEHRPKIK++HPGL
dna-binding     95  EDMAKSDKARYDREMKNYVPPKGDKKGKKKDPNAPKRPPSAFFLCSEHRPKIKSEHPGL 120
dna-binding     61  *****
HMG2            61  ++++++

Query:          121 SIGDTAKKLGEWSEQLAKDKQPYEQKAAKLKEYEKDIAAYRAKSKSDAGKKGPRPAG 180
Sbjct:          121 SIGDTAKKLGEWSEQ AKDKQPYEQKAAKLKEYEKDIAAYRAK  KS+AGKKGPRP  G
Conflict        163  SIGDTAKKLGEWSEQSAKDKQPYEQKAAKLKEYEKDIAAYRAK  KSEAGKKGPRPTG 180
dna-binding     121  *****
HMG2            121  ++++++

Query:          181 SKKKAPEEEEEEEEEEEEEEEEEDEE 207
Sbjct:          181 SKKK  EPE+EEEEEE+E+E+EEEEDE+
ASP/GLU-RICH (ACIDIC) 186 SKKKNEPEEEEEEEEEEEEEDEE 207
HMG2            181 *****
                181 ++++++
  
```

CPU time: 0.06 user secs. 0.03 sys. secs 0.09 total secs.

Lambda K H
 0.304 0.126 0.358

Gapped
 Lambda K H
 0.267 0.0410 0.140

Matrix: BLOSUM62

Gap Penalties: Existence: 11, Extension: 1